

SEQUENCE LISTING

<110> Gentide Biopharmaceuticals, Inc.  
Bussell, Stuart

<120> METHODS TO CONSTRUCT MULTIMERIC DNA AND POLYMERIC PROTEIN SEQUENCES AS  
DIRECT FUSIONS OR WITH LINKERS

<130> GNT-00101.P.1-US

<150> US 60/396,466  
<151> 2002-07-16

<160> 86

<170> PatentIn version 3.0

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Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro  
35 40 45

Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg  
50 55 60

Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu  
65 70 75 80

Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val  
85 90 95

Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp  
100 105 110

Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu  
115 120 125

Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser  
130 135 140

Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr  
145 150 155 160

Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe  
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Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
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Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
100 105 110

Asp Leu Leu Lys Asp Leu Glu Gly Ile Gln Thr Leu Met Gly Arg  
115 120 125

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130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
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Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
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Thr Val Ala Gln Ala  
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120

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Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr  
35 40 45

Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser  
50 55 60

Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro  
65 70 75 80

Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu  
85 90 95

Leu Arg Ile Ser Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln  
100 105 110

Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp  
115 120 125

Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr  
130 135 140

Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe  
145 150 155 160

Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala  
165 170 175

Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp  
180 185 190

Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly

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205

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Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
 35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
 50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
 65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly  
180 185

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gaaggcctata tcccaaagga acagaagtat tcattcctgc agaacccccac gaccccttc 180

tgtttctcag agtctattcc gacaccctcc aacaggagg aaacacaaca gaaatccac 240

ctagagctgc tccgcacatc cctgctgctc atccagtcgt ggctggagcc cgtgcagttc 300

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Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe  
35 40 45

Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr  
50 55 60

Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu  
65 70 75 80

Arg Ile Ser Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe  
85 90 95

Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser  
100 105 110

Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu  
115 120 125

Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys  
130 135 140

Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu  
145 150 155 160

Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys  
165 170 175

Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly  
180 185 190

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tccaacagg	aggaaacaca	acagaaatcc	aacctagac	tgctccgc	ctccctgctg	840
ctcatccagt	cgtggctgga	gcccgtgcag	ttcctcagga	gtgtcttcgc	caacagcc	900
gtgtacggcg	cctctgacag	caacgtctat	gacccctaa	aggacctaga	ggaaggcatc	960
caaacgctga	tggggaggct	ggaagatggc	agccccgg	ctgggcagat	cttcaagcag	1020
acctacagca	agttcgacac	aaactcacac	aacgatgacg	cactactcaa	gaactacggg	1080
ctgctctact	gttcaggaa	ggacatggac	aaggtcgaga	cattcctgc	catcgtcag	1140
tgccgctctg	tggagggatc	c				1161

<210> 27  
 <211> 382  
 <212> PRT  
 <213> Artificial

<220>  
 <223> synthetic sequence

<400> 27

Ser Cys Gly Phe Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn  
 1 5 10 15

Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr  
 20 25 30

Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe  
 35 40 45

Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr  
50 55 60

Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu  
65 70 75 80

Arg Ile Ser Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe  
85 90 95

Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser  
100 105 110

Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu  
115 120 125

Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys  
130 135 140

Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu  
145 150 155 160

Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys  
165 170 175

Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser  
180 185 190

Cys Gly Phe Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala  
195 200 205

Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln  
210 215 220

Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu  
225 230 235 240

Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro  
245 250 255

Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg  
260 265 270

Ile Ser Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu  
275 280 285

Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn  
290 295 300

Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met  
305 310 315 320

Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln  
325 330 335

Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu  
340 345 350

Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val  
355 360 365

Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly  
370 375 380

<210> 28

<211> 1152

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> misc\_feature

<222> (574)..(1146)

<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 28

tgatcatgtg gcttcttccc aaccattccc ttatccaggc ttttgacaa cgctatgctc 60

cgcgcccatc gtctgcacca gctggcctt gacacctacc aggagttga agaagcctat 120

atcccaaagg aacagaagta ttcattcctg cagaacccccc agacctccct ctgtttctca 180

gagtctattc cgacaccctc caacagggag gaaacacaac agaaatccaa cctagagctg 240

ctccgcattt ccctgctgct catccagtcg tggctggagc cctgcagtt cctcaggagt 300

gttttcgcca acagcctgggt gtacggcgcc tctgacagca acgtctatga cctcctaaag 360

gacctagagg aaggcatcca aacgctgatg gggaggctgg aagatggcag ccccccggact 420

ggccagatct tcaaggcagac ctacagcaag ttcgacacaaa actcacacaa cgtgacgca 480

ctactcaaga actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca 540

ttcctgcgca tcgtgcagtg ccgcctgtg gagggatcat gtggttttt cccaccatt 600

cccttatcca ggcttttga caacgctatg ctccgcgccc atcgtctgca ccagctggcc 660

tttgacacct accaggagtt tgaagaagcc tatatccaa aggaacagaa gtattcattc 720

ctgcagaacc cccagacctc cctctgtttc tcagagtcta ttccgacacc ctccaacagg 780

gaggaaacac aacagaaatc caacctagag ctgctccgca tctccctgct gctcatccag 840

tcgtggctgg agccctgtca gttcctcagg agtgtctcg ccaacagcct ggtgtacggc 900

gcctctgaca gcaacgtcta tgacacctta aaggacctag aggaaggcat ccaaacgctg 960

atggggaggc tggaagatgg cagccccgg actgggcaga tcttcaagca gacctacagc 1020

aagttcgaca caaactcaca caacgatgac gcactactca agaactacgg gctgctctac 1080

tgcttcagga aggacatgga caaggtcgag acattcctgc gcatcgtgca gtgccgctct 1140

gtggaggat cc 1152

<210> 29

<211> 382

<212> PRT

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> MISC\_FEATURE

<222> (191)..(381)

<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 29

Ser Cys Gly Phe Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn  
1 5 10 15

Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr  
20 25 30

Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe  
35 40 45

Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr  
50 55 60

Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu  
65 70 75 80

Arg Ile Ser Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe  
85 90 95

Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser  
100 105 110

Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu  
115 120 125

Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys  
130 135 140

Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu  
145 150 155 160

Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys  
165 170 175

Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser

180	185	190
Cys Gly Phe Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala		
195	200	205
Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln		
210	215	220
Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu		
225	230	235
240		
Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro		
245	250	255
Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg		
260	265	270
Ile Ser Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu		
275	280	285
Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn		
290	295	300
320		
Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met		
305	310	315
325		
Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln		
330		
335		
Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu		
340	345	350
Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val		
355	360	365
Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly		
370	375	380
<210> 30		
<211> 606		
<212> DNA		
<213> Artificial		
<220>		
<223> synthetic sequence		
<400> 30		
catatgttcc caaccattcc cttatccagg ctttttgcaca acgctatgct ccgcgcctat	60	
cgtctgcacc agctggcctt tgacacctac caggagttt aagaaggctt tattccaaag	120	
gaacagaagt attcattcct gcagaacccc cagacccccc tctgtttctc agagtctatt	180	
ccgacaccct ccaacagggg gaaacacaa cagaaatcca accttagagct gctccgcattc	240	
tcctgtgc tcatccagtc gtggctggag cccgtgcagt tcctcaggag tgtcttcgccc	300	

aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag 360  
gaaggcatcc aaacgctgat gggaggctg gaagatggca gccccggac tggcagatc 420  
ttcaagcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag 480  
aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc 540  
atcgtcagt gccgctctgt ggagggatcc gaattccatt gatcatgtgg cttctagtag 600  
gtcgac 606

<210> 31  
<211> 1737  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<220>  
<221> misc\_feature  
<222> (1138)..(1710)  
<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 31  
catatgttcc caaccattcc cttatccagg cttttgaca acgctatgct ccgcgcctat 60  
cgtctgcacc agctggcctt tgacacccatc caggagttt aagaagccta tatcccaaag 120  
gaacagaagt attcattccct gcagaacccc cagacccccc tctgtttctc agagtctatt 180  
ccgacaccct ccaacagggaa ggaaacacaa cagaaatcca acctagagct gctccgcattc 240  
tccctgtgc tcattccagtc gtggctggag cccgtcagt tcctcaggag tgtcttcgcc 300  
aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag 360  
gaaggcatcc aaacgctgat gggaggctg gaagatggca gccccggac tggcagatc 420  
ttcaagcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag 480  
aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc 540  
atcgtcagt gccgctctgt ggagggatca tgtggcttct tcaccatccat tcccttatcc 600  
aggcttttgc acaacgctat gctccgcgc catcgctgc accagctggc ctttgacacc 660  
taccaggagt ttgaagaagc ctatatccca aaggaacaga agtattcatt cctgcagaac 720  
ccccagaccc cccctgttt ctcagagtct attccgacac cctccaaacag ggagggaaaca 780  
caacagaaat ccaacctaga gctgctccgc atctccctgc tgctcatcca gtcgtggctg 840

gagcccggtgc agttcctcag gagtgcttc gccaacagcc tgggtacgg cgctctgac 900  
agcaacgtct atgacctcct aaaggaccta gaggaaggca tccaaacgct gatggggagg 960  
ctggaagatg gcagcccccg gactggcag atcttcaagc agacctacag caagttcgac 1020  
acaaactcac acaacgatga cgcaactac aagaactacg ggctgctcta ctgcttcagg 1080  
aaggacatgg acaagggtcga gacattcctg cgcatcggtc agtgccgctc tgtggaggga 1140  
tcatgtggct tttcccaac cattccctta tccaggctt ttgacaacgc tatgctccgc 1200  
gccccatcgtc tgccaccaact ggcccttgac acctaccagg agtttgaaga agcctatatac 1260  
ccaaaggaac agaagtattc attcctgcag aaccccccaga cctccctctg tttctcagag 1320  
tctattccga caccctccaa cagggaggaa acacaacaga aatccaacct agagctgctc 1380  
cgcatctccc tgctgctcat ccagtcgtgg ctggagcccg tgcaagttcct caggagtgtc 1440  
ttcgccaaca gcctgggtgtc cggcgctct gacagcaacg tctatgacct cctaaaggac 1500  
ctagaggaag gcatccaaac gctgatgggg aggctggaag atggcagccc ccggactggg 1560  
cagatcttca agcagaccta cagcaagttc gacacaaact cacacaacga tgacgcacta 1620  
ctcaagaact acgggctgct ctactgcttc aggaaggaca tggacaaggt cgagacattc 1680  
ctgcgcacatcg tgcaagtggcct ctctgtggag ggatcatgtg gcttctagta ggtcgac 1737

<210> 32  
<211> 574  
<212> PRT  
<213> Artificial

<220>  
<223> synthetic sequence

<220>  
<221> MISC\_FEATURE  
<222> (379)..(569)  
<223> sequence is repeated N-1 times, where N is a positive whole number

<220>  
<221> mat\_peptide  
<222> (1)..()

<400> 32

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu  
1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe  
20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
180 185 190

Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg  
195 200 205

Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu  
210 215 220

Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro  
225 230 235 240

Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg  
245 250 255

Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu  
260 265 270

Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val  
275 280 285

Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp  
290 295 300

Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu  
305 310 315 320

Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser  
325 330 335

Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr  
340 345 350

Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe  
355 360 365

Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Phe  
370 375 380

Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala  
385 390 395 400

His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu  
405 410 415

Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln  
420 425 430

Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu  
435 440 445

Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu  
450 455 460

Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe  
465 470 475 480

Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu  
485 490 495

Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu  
500 505 510

Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys  
515 520 525

Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly  
530 535 540

Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu  
545 550 555 560

Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
565 570

<210> 33  
<211> 55  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 33  
taccatatga catgatcatg tggcttcgggt ttcccaacca ttcccttatac caggc 55

<210> 34  
<211> 591  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 34  
catatgacat gatcatgtgg ctccggtttc ccaaccattc ccttatccag gcttttgac 60  
aacgctatgc tccgcgcccc tcgtctgcac cagctggcct ttgacaccta ccaggagttt 120  
gaagaaggcct atatccaaa ggaacagaag tattcattcc tgcaagaaccc ccagacacctc 180  
ctctgtttct cagagtctat tccgacaccc tccaaacaggg aggaaacaca acagaaatcc 240  
aacctagagc tgctccgcat ctccctgctg ctcatccagt cgtggctgga gcccgtgcag 300  
ttcctcagga gtgtcttcgc caacagcctg gtgtacggcg cctctgacag caacgtctat 360  
gacccctaa aggacctaga ggaaggcatc caaacgctga tggggaggct ggaagatggc 420  
agcccccgga ctggcagat cttcaagcag acctacagca agttcgacac aaactcacac 480  
aacgatgacg cactactcaa gaactacggg ctgctctact gcttcaggaa ggacatggac 540  
aaggtcgaga cattcctgcg catcgtgcag tgccgctctg tggagggate c 591

<210> 35  
<211> 192  
<212> PRT  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 35

Ser Cys Gly Phe Gly Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp  
1 5 10 15

Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr  
20 25 30

Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser  
35 40 45

Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro  
50 55 60

Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu  
65 70 75 80

Leu Arg Ile Ser Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln

85

90

95

Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp  
 100 105 110

Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr  
 115 120 125

Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe  
 130 135 140

Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala  
 145 150 155 160

Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp  
 165 170 175

Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly  
 180 185 190

&lt;210&gt; 36

&lt;211&gt; 1158

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; synthetic sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (577)..(1152)

&lt;223&gt; sequence is repeated N-1 times, where N is a positive whole number

&lt;400&gt; 36

tgatcatgtg gcttcggttt cccaaaccatt cccttatcca ggcttttga caacgctatg 60

ctccgcgccc atcgtctgca ccagctggcc tttgacacacct accaggagtt tgaagaagcc 120

tatatatccaa aggaacagaa gtattcattc ctgcagaacc cccagacctc cctctgttcc 180

tcagagtcta ttccgacacc ctccaacagg gagaaacac aacagaaatc caacctagag 240

ctgctccgca tctccctgct gctcatccag tcgtggctgg agcccgtgca gttcctcagg 300

agtgtcttcg ccaacagcct ggtgtacggc gcctctgaca gcaacgtcta tgacctccata 360

aaggacctag aggaaggcat ccaaacgctg atggggaggc tggaagatgg cagccccgg 420

actggcaga tcttcaagca gacctacagc aagttcgaca caaactcaca caacgatgac 480

gcactactca agaactacgg gctgctctac tgcttcagga aggacatgga caaggtcgag 540

acattcctgc gcatcgtgca gtgccgtct gtggagggat catgtggctt cggtttccca 600

accattccct tatccaggct ttttgacaac gctatgctcc gcgcccatcg tctgcaccag 660

ctggccttg acacctacca ggagttgaa gaagcctata tcccaaagga acagaagtat 720  
tcattcctgc agaacccca gaccccttc tgtttctcag agtctattcc gacaccctcc 780  
aacaggagg aaacacaaca gaaatccaac ctagagctgc tccgcacatctc cctgctgctc 840  
atccagtcgt ggctggagcc cgtgcagttc ctcaggagtg tcttcgcca cagcctgg 900  
tacggcgct ctgacagcaa cgctatgac ctcctaaagg acctagagga aggcatacaa 960  
acgctgatgg ggaggctgga agatggcagc cccggactg ggcagatctt caagcagacc 1020  
tacagcaagt tcgacacaaa ctcacacaac gatgacgcac tactcaagaa ctacggctg 1080  
ctctactgct tcaggaagga catggacaag gtcgagacat tcctgcgc cat cgtcagtc 1140  
cgctctgtgg agggatcc 1158

<210> 37

<211> 384

<212> PRT

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> MISC\_FEATURE

<222> (192)..(383)

<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 37

Ser Cys Gly Phe Gly Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp  
1 5 10 15

Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr  
20 25 30

Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser  
35 40 45

Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro  
50 55 60

Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu  
65 70 75 80

Leu Arg Ile Ser Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln  
85 90 95

Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp  
100 105 110

Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr  
115 120 125

Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe  
130 135 140

Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala  
145 150 155 160

Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp  
165 170 175

Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly  
180 185 190

Ser Cys Gly Phe Gly Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp  
195 200 205

Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr  
210 215 220

Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser  
225 230 235 240

Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro  
245 250 255

Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu  
260 265 270

Leu Arg Ile Ser Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln  
275 280 285

Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp  
290 295 300

Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr  
305 310 315 320

Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe  
325 330 335

Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala  
340 345 350

Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp  
355 360 365

Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly  
370 375 380

<210> 38  
<211> 1743  
<212> DNA  
<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> misc\_feature

<222> (1141)..(1716)

<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 38

catatgttcc	caaccattcc	cttacccagg	cttttgaca	acgttatgct	ccgcgcctat	60
cgtctgcacc	agctggcctt	tgacacctac	caggagttt	aagaaggcta	tatcccaaag	120
gaacagaagt	attcattcct	gcagaacccc	cagacctccc	tctgtttctc	agagtctatt	180
ccgacacccct	ccaacaggga	gaaacaccaa	cagaatcca	acctagagct	gtccgcac	240
tccctgctgc	tcatccagtc	gtggctggag	cccggtcagt	tcctcaggag	tgtcttcg	300
aacagcctgg	tgtacggcgc	ctctgacagc	aacgtctatg	accccttaaa	ggacctagag	360
gaaggcatcc	aaacgctgat	ggggaggctg	gaagatggca	ccccccggac	tggcagatc	420
ttcaagcaga	cctacagcaa	gttcgacaca	aactcacaca	acgtgacgc	actactcaag	480
aactacgggc	tgctctactg	cttcaggaag	gacatggaca	aggtcgagac	attcctgcgc	540
atcgtgcagt	gccgctctgt	ggagggatca	tgtggcttcg	gtttcccaac	cattccctta	600
tccaggcttt	ttgacaacgc	tatgtccgc	gcccatcg	tgaccagac	ggccttgac	660
acctaccagg	agtttgaaga	agcctatatac	ccaaaggaac	agaagtattc	attcctgcag	720
aaccccccaga	cctccctctg	tttctcagag	tctattccga	caccctccaa	cagggaggaa	780
acacaacaga	aatccaacct	agagctgctc	cgcacatccc	tgctgctcat	ccagtcgtgg	840
ctggagcccg	tgcagttcct	caggagtgtc	ttcgccaaca	gcctggtgta	cggcgctct	900
gacagcaacg	tctatgacct	cctaaaggac	ctagaggaag	gcacccaaac	gctgatgggg	960
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gacacaaact	cacacaacga	tgacgcacta	ctcaagaact	acgggctgct	ctactgcttc	1080
aggaaggaca	tggacaaggt	cgagacattc	ctgcgcac	tgcagtggcg	ctctgtggag	1140
ggatcatgtg	gcttcggttt	cccaaccatt	cccttatcca	ggcttttga	caacgctatg	1200
ctccgcgccc	atcgtctgca	ccagctggcc	tttgacacct	accaggagtt	tgaagaagcc	1260
tatatcccaa	aggaacagaa	gtattcattc	ctgcagaacc	cccagacctc	cctctgtttc	1320
tcagagtcta	ttccgacacc	ctccaacagg	gaggaaacac	aacagaaatc	caacctagag	1380

ctgctccgca tctccctgct gctcatccag tcgtggctgg agcccggtca gttcctcagg 1440  
agtgtcttcg ccaacagcct ggtgtacggc gcctctgaca gcaacgtcta tgacccctca 1500  
aaggacctag aggaaggcat ccaaacgctg atggggaggc tggaaagatgg cagccccgg 1560  
actggcaga tcttcaagca gacctacagc aagttcgaca caaactcaca caacgatgac 1620  
gcactactca agaactacgg gctgctctac tgcttcagga aggacatgga caaggtcgag 1680  
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gac 1743

<210> 39  
<211> 576  
<212> PRT  
<213> Artificial

<220>  
<223> synthetic sequence

<220>  
<221> MISC\_FEATURE  
<222> (380)..(571)  
<223> sequence is repeated N-1 times, where N is a positive whole number

<220>  
<221> mat\_peptide  
<222> (1)..()

<400> 39

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu  
1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe  
20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
180 185 190

Gly Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu  
195 200 205

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe  
210 215 220

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
225 230 235 240

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
245 250 255

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
260 265 270

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
275 280 285

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
290 295 300

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
305 310 315 320

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
325 330 335

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
340 345 350

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
355 360 365

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
370 375 380

Gly Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu  
385 390 395 400

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe  
405 410 415

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
420 425 430

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
435 440 445

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
450 455 460

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
465 470 475 480

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
485 490 495

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
500 505 510

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
515 520 525

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
530 535 540

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
545 550 555 560

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
565 570 575

<210> 40

<211> 39

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<400> 40

cgccggatcct catgagaagc cacagctgcc ctccacaga 39

<210> 41

<211> 591

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<400> 41

catatgttcc caaccattcc cttatccagg ctttttgaca acgctatgct ccgcgcctat 60

cgtctgcacc agctggcctt tgacacacctac caggagtttg aagaagccta tatcccaaag 120

gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt 180

ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gctccgcac	240
tccctgctgc tcataccagtc gtggctggag cccgtgcagt tcctcaggag tgcgttcgccc	300
aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag	360
gaaggcatcc aaacgctgat gggaggctg gaagatggca gccccggac tggcagatc	420
ttcaagcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag	480
aactacgggc tgctctactg cttaggaag gacatggaca aggtcgagac attcctgcgc	540
atcgtgcagt gcccgtctgt ggagggcagc tgcgtttct catgaggatc c	591

<210> 42  
 <211> 193  
 <212> PRT  
 <213> Artificial

<220>  
 <223> synthetic sequence

<400> 42

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu			
1	5	10	15
10	15		

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe			
20	25	30	
30			

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn			
35	40	45	
45			

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn			
50	55	60	
60			

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser			
65	70	75	80
75	80		

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser			
85	90	95	
95			

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr			
100	105	110	
110			

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg			
115	120	125	
125			

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr			
130	135	140	
140			

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn			
145	150	155	160
155	160		

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr			
165	170	175	
175			

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
180 185 190

Ser

<210> 43  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 43  
catgccatgg ggtggtgag gaagtttccc aaccattccc ttatccaggc 50

<210> 44  
<211> 606  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 44  
ccatgggtg gtggaggaag tttcccaacc attcccttat ccaggcttt tgacaacgct 60  
atgctccgcg cccatcgct gcacccagctg gcctttgaca cctaccagga gtttgaagaa 120  
gcctatatcc caaaggaaca gaagtattca ttcctgcaga acccccagac ctccctctgt 180  
ttctcagagt ctattccgac accctccaac agggaggaaa cacaacagaa atccaaccta 240  
gagctgctcc gcatctccct gctgctcatac cagtcgtggc tggagcccggt gcagttcctc 300  
aggagtgtct tcgccaacag cctgggtgtac ggccgcctctg acagcaacgt ctatgacctc 360  
ctaaaggacc tagaggaagg catccaaacg ctgatggga ggctggaaga tggcagcccc 420  
cggaactggc agatcttcaa gcagacctac agcaagttcg acacaaaactc acacaacgat 480  
gacgcactac tcaagaacta cgggctgctc tactgcttca ggaaggacat ggacaaggtc 540  
gagacattcc tgcgcatacg tgcgtggagg gcagctgtgg cttctcatga 600  
ggatcc 606

<210> 45  
<211> 198  
<212> PRT  
<213> Artificial

<220>

<223> synthetic sequence

<400> 45

Trp Gly Gly Gly Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe  
1 5 10 15

Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp  
20 25 30

Thr Tyr Gln Glu Phe Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr  
35 40 45

Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile  
50 55 60

Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu  
65 70 75 80

Leu Leu Arg Ile Ser Leu Leu Ile Gln Ser Trp Leu Glu Pro Val  
85 90 95

Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser  
100 105 110

Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln  
115 120 125

Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile  
130 135 140

Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp  
145 150 155 160

Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met  
165 170 175

Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu  
180 185 190

Gly Ser Cys Gly Phe Ser  
195

<210> 46

<211> 603

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<400> 46

ccatggggtg gtggaggaag tttcccaacc attcccttat ccaggcttt tgacaacgct 60

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gcctatatcc caaaggaaca gaagtattca ttccctgcaga acccccagac ctccctctgt 180

ttctcagagt ctattccgac accctccaac agggaggaaa cacaacagaa atccaaccta 240  
gagctgctcc gcatctccct gctgctcatc cagtcgtggc tggagcccgt gcagttccctc 300  
aggagtgtct tcgccaacag cctgggtgtac ggccgcctctg acagcaacgt ctatgacctc 360  
ctaaaggacc tagaggaagg catccaaacg ctgatgggga ggctggaaga tggcagcccc 420  
cggaactgggc agatcttcaa gcagacctac agcaagttcg acacaaactc acacaacgat 480  
gacgcactac tcaagaacta cgggctgctc tactgcttca ggaaggacat ggacaaggtc 540  
gagacattcc tgcgcattcgt gcagtgccgc tctgtggagg gcagctgtgg cttctaggg 600  
tcc 603

<210> 47  
<211> 197  
<212> PRT  
<213> Artificial

<220>  
<223> synthetic sequence  
<400> 47

Trp Gly Gly Gly Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe  
1 5 10 15

Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp  
20 25 30

Thr Tyr Gln Glu Phe Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr  
35 40 45

Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile  
50 55 60

Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu  
65 70 75 80

Leu Leu Arg Ile Ser Leu Leu Ile Gln Ser Trp Leu Glu Pro Val  
85 90 95

Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser  
100 105 110

Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln  
115 120 125

Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile  
130 135 140

Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp  
145 150 155 160

Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met  
165 170 175

Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu  
180 185 190

Gly Ser Cys Gly Phe  
195

<210> 48  
<211> 1200  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<220>  
<221> misc\_feature  
<222> (595)..(1188)  
<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 48  
ccatggggtg gtggaggaag tttcccaacc attcccttat ccaggcttt tgacaacgct 60  
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gcctatatcc caaaggaaca gaagtattca ttcctgcaga acccccagac ctccctctgt 180  
ttctcagagt ctattccgac accctccaac agggaggaaa cacaacagaa atccaaccta 240  
gagctgctcc gcatctccct gctgctcatc cagtcgtggc tggagcccgt gcagttcctc 300  
aggagtgtct tcgccaacag cctggtgtac ggcgcctctg acagcaacgt ctatgacctc 360  
ctaaaggacc tagaggaagg catccaaacg ctgatggga ggctggaaga tggcagcccc 420  
cggaactggc agatctcaa gcagaccta agcaagttcg acacaaactc acacaacgat 480  
gacgcactac tcaagaacta cgggctgctc tactgcttca ggaaggacat ggacaaggtc 540  
gagacattcc tgcgcattcg gtcaatgcgc tctgtggagg gcagctgtgg cttctatgg 600  
ggtgtggag gaagttccc aaccattccc ttatccaggc tttttgacaa cgctatgctc 660  
cgcccccattc gtctgcacca gctggcctt gacacctacc aggagttga agaaggctat 720  
atcccaaagg aacagaagta ttcatccctg cagaaccccc agacccctt ctgtttctca 780  
gagtttattc cgacaccctc caacagggag gaaacacaac agaaatccaa cctagagctg 840  
ctccgcattt ccctgctgtt catccagtcg tggctggagc ccgtgcagtt cctcaggagt 900  
gtcttcgcca acagccttgtt gtacggcgcc tctgacagca acgtctatga cctcctaaag 960

gacc tagagg aagg catcca aacg ctgatg gggagg ctgg aagatggcag cccccc ggact 1020  
ggcagatct tcaagc agac ctac agcaag ttgc acac aac actc acac aac cgatg acgca 1080  
ctactcaaga actac gggct gctctactgc ttca ggaagg acatggacaa ggtc gagaca 1140  
ttcctgcgca tcgtgc agtg ccgctctgtg gagggc agct gtggcttctc atgaggatcc 1200

<210> 49  
<211> 396  
<212> PRT  
<213> Artificial

<220>  
<223> synthetic sequence

<220>  
<221> MISC\_FEATURE  
<222> (198) .. (395)  
<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 49

Trp Gly Gly Gly Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe  
1 5 10 15

Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp  
20 25 30

Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr  
35 40 45

Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile  
50 55 60

Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu  
65 70 75 80

Leu Leu Arg Ile Ser Leu Leu Ile Gln Ser Trp Leu Glu Pro Val  
85 90 95

Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser  
100 105 110

Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln  
115 120 125

Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile  
130 135 140

Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp  
145 150 155 160

Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met  
165 170 175

Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu  
180 185 190

Gly Ser Cys Gly Phe Ser Trp Gly Gly Gly Ser Phe Pro Thr Ile  
195 200 205

Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu  
210 215 220

His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile  
225 230 235 240

Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu  
245 250 255

Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln  
260 265 270

Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Ile Gln  
275 280 285

Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser  
290 295 300

Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp  
305 310 315 320

Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser  
325 330 335

Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr  
340 345 350

Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr  
355 360 365

Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val  
370 375 380

Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Ser  
385 390 395

<210> 50  
<211> 1185  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 50  
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cgtctgcacc agctggcctt tgacacctac caggagttg aagaagccta tatcccaaag 120

gaacagaagt attcattcct gcagaacccc cagacctccc tctgttctc agagtctatt 180  
ccgacacccct ccaacaggga ggaaacacaa cagaaatcca accttagagct gctccgcattc  
tccctgctgc tcatccagtc gtggctggag cccgtgcagt tcctcaggag tgtcttcgccc  
aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag 300  
gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc  
ttcaaggcaga cctacagcaa gttcgacaca aactcacaca acgtgacgc actactcaag 360  
aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc  
atcgtgcagt gccgctctgt ggagggcagc tggcttct catggggtgg tggaggaagt 420  
ttcccaacca ttcccttatac caggctttt gacaacgcta tgctccgcgc ccatcgctcg  
caccagctgg ccttgacac ctaccaggag tttgaagaag cctatatccc aaaggaacag 480  
aagtattcat tcctgcagaa ccccgagacc tccctctgtt tctcagagtc tattccgaca  
ccctccaaca gggagggaaac acaacagaaa tccaacctag agctgctccg catctccctg  
ctgctcatcc agtcgtggct ggagcccggt cagttcctca ggagtgtctt cgccaaacagc  
ctggtgtacg gcgcctctga cagcaacgtc tatgacacctc taaaggacct agaggaaggc  
atccaaacgc tcatggggag gctggaagat ggcagcccc ggactggca gatcttcaag 540  
cagacctaca gcaagttcga cacaaactca cacaacgatg acgcactact caagaactac  
gggctgctct actgcttcag gaaggacatg gacaaggatcg agacattcct ggcgcattcg  
cagtqccqct ctgtqqaqqq caqctgtggc ttctcatgat gatcc 600  
1140  
1185

<210> 51  
<211> 391  
<212> PRT  
<213> Artificial

<220>  
<223> synthetic sequence

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<220>
<221>  mat_peptide
<222>  (1)..()
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<400> 51

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu  
1 5 10 15

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
100 105 110

Asp Leu Leu Lys Asp Leu Glu Gly Ile Gln Thr Leu Met Gly Arg  
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
180 185 190

Ser Trp Gly Gly Gly Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu  
195 200 205

Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe  
210 215 220

Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys  
225 230 235 240

Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser  
245 250 255

Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu  
260 265 270

Glu Leu Leu Arg Ile Ser Leu Leu Ile Gln Ser Trp Leu Glu Pro  
275 280 285

Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala  
290 295 300

Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile  
305 310 315 320

Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln  
325 330 335

Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp  
340 345 350

Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp  
355 360 365

Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val  
370 375 380

Glu Gly Ser Cys Gly Phe Ser  
385 390

<210> 52  
<211> 1779  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<220>  
<221> misc\_feature  
<222> (1174) .. (1767)  
<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 52  
catatgttcc caaccattcc cttatccagg cttttgaca acgctatgct ccgcgcctat 60  
cgtctgcacc agctggcctt tgacacctac caggagttt aagaagccta tatcccaaag 120  
gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt 180  
ccgacaccct ccaacaggga ggaaacacaa cagaaatcca acctagagct gctccgcattc 240  
tccctgctgc tcatccagtc gtggctggag cccgtgcagt tcctcaggag tgtcttcgccc 300  
aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag 360  
gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc 420  
ttcaaggcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag 480  
aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc 540  
atcgtgcagt gccgctctgt ggagggcagc tgtggcttct catgggtgg tggaggaagt 600  
ttcccaacca ttcccttatac caggctttt gacaacgcta tgctccgcgc ccatcgtctg 660  
caccagctgg ccttgacac ctaccaggag tttgaagaag cctatatccc aaaggaacag 720  
aagtattcat tcctgcagaa cccccagacc tccctctgtt tctcagagtc tattccgaca 780  
ccctccaaca gggagggaaac acaacagaaa tccaaacctag agctgctccg catctccctg 840

ctgctcatcc agtcgtggct ggagcccgta cagttcctca ggagtgtctt cgccaaacagc	900
ctggtgtacg gcgcctctga cagcaacgtc tatgacctcc taaaggacct agaggaaggc	960
atccaaacgc tgatggggag gctggaagat ggcagccccc ggactggca gatcttcaag	1020
cagacctaca gcaagttcga cacaactca cacaacgatg acgcactact caagaactac	1080
gggctgctct actgcttcag gaaggacatg gacaaggctcg agacattcct gcgcatcgtg	1140
cagtgcgcgt ctgtggaggg cagctgtggc ttctcatggg gtggtgagg aagtttccca	1200
accattccct tatccaggct ttttgcacaac gctatgctcc ggcgcattcg tctgcaccag	1260
ctggcctttg acacctacca ggagttgaa gaagcctata tcccaaagga acagaagtg	1320
tcattcctgc agaaccggca gaccccttc tggttctcag agtctattcc gacaccctcc	1380
aacagggagg aaacacaaca gaaatccaac cttagagctgc tccgcatttc cctgctgctc	1440
atccagtcgt ggctggagcc cgtcagttc ctcaggatgt tcttcgccaa cagcctggtg	1500
tacggcgct ctgacagcaa cgtctatgac ctcctaaagg acctagagga aggcattccaa	1560
acgctgatgg ggaggctgga agatggcagc ccccgactg ggcagatctt caagcagacc	1620
tacagcaagt tcgacacaaa ctcacacaac gatgacgcac tactcaagaa ctacggctg	1680
ctctactgct tcaggaagga catggacaag gtcgagacat tcctgcgcatt cgtcagtg	1740
cgctctgtgg agggcagctg tggcttctca tqaqqatcc	1779

<210> 53  
<211> 589  
<212> PRT  
<213> Artificial

<220>  
<223> synthetic sequence

<220>  
<221> MISC FEATURE  
<222> (391)..(588)  
<223> sequence is repeated N-1 times, where N is a positive whole number

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<220>
<221>  mat_peptide
<222>  (1)..()
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<400> 53

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu  
1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe  
20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
180 185 190

Ser Trp Gly Gly Gly Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu  
195 200 205

Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe  
210 215 220

Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys  
225 230 235 240

Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser  
245 250 255

Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu  
260 265 270

Glu Leu Leu Arg Ile Ser Leu Leu Ile Gln Ser Trp Leu Glu Pro  
275 280 285

Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala  
290 295 300

Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile  
305 310 315 320

Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln  
325 330 335

Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp  
340 345 350

Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp  
355 360 365

Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val  
370 375 380

Glu Gly Ser Cys Gly Phe Ser Trp Gly Gly Gly Ser Phe Pro Thr  
385 390 395 400

Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala His Arg  
405 410 415

Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr  
420 425 430

Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser  
435 440 445

Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr  
450 455 460

Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Ile  
465 470 475 480

Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn  
485 490 495

Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys  
500 505 510

Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly  
515 520 525

Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp  
530 535 540

Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu  
545 550 555 560

Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile  
565 570 575

Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Ser  
580 585

<210> 54  
<211> 2370  
<212> DNA  
<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> misc\_feature

<222> (1174)..(1767)

<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 54  
catatgttcc caaccattcc cttatccagg cttttgaca acgctatgct ccgcgcggcat 60  
cgtctgcacc agctggcctt tgacacctac caggagttt aagaaggcta tatcccaaag 120  
gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt 180  
ccgacaccct ccaacaggga gcaaacacaa cagaaatcca acctagagct gctccgcac 240  
tccctgctgc tcattccagtc gtggctggag cccgtgcagt tcctcaggag tgtcttcgccc 300  
aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag 360  
gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccccggac tgggcagatc 420  
ttcaaggcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag 480  
aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc 540  
atcgtgcagt gccgcctctgt ggagggcagc tgtggcttct catgggggtgg tggaggaagt 600  
ttcccaacca ttcccttatac caggctttt gacaacgcta tgctccgcgc ccattcgtctg 660  
caccagctgg ccttgacac ctaccaggag tttgaagaag cctatatccc aaaggaacag 720  
aagtattcat tcctgcagaa cccccagacc tccctctgtt tctcagagtc tattccgaca 780  
ccctccaaca gggagggaaac acaacagaaa tccaacctag agctgctccg catctccctg 840  
ctgctcatcc agtcgtggct ggagcccggtg cagttcctca ggagtgtctt cgccaaacagc 900  
ctggtgtacg ggcgccttga cagcaacgtc tatgacctcc taaaggacct agaggaaggc 960  
atccaaacgc tggatggggag gctggaagat ggcagcccc ggactgggca gatcttcaag 1020  
cagacctaca gcaagttcga cacaactca cacaacgatg acgcactact caagaactac 1080  
gggctgtct actgcttcag gaaggacatg gacaaggctcg agacattcct ggcgcattctg 1140  
cagtgcccgct ctgtggaggg cagctgtggc ttctcatggg gtgggtggagg aagtttccca 1200  
accattccct tatccaggct ttttgcacac gctatgtcc ggcgcctatcg tctgcaccag 1260  
ctggcccttg acacctacca ggagttgaa gaagcctata tcccaaagga acagaagttat 1320  
tcattcctgc agaacccttca gaccccttc tggatctcag agtctattcc gacaccctcc 1380  
aacagggagg aaacacaaca gaaatccaaac ctagagctgc tccgcatttc cctgctgctc 1440

atccagtcgt ggctggagcc cgtgcagttc ctcaggagtg tcctcgccaa cagoctggtg 1500  
tacggcgccct ctgacagcaa cgtctatgac ctcctaaagg acctagagga aggcattccaa 1560  
acgctgatgg ggaggctgga agatggcagc ccccgactg ggcagatctt caagcagacc 1620  
tacagcaagt tcgacacaaa ctcacacaac gatgacgcac tactcaagaa ctacgggctg 1680  
ctctactgct tcaggaagga catggacaag gtcgagacat tcctgcgcac cgtgcagtgc 1740  
cgctctgtgg agggcagctg tggcttctca tgggtggtg gaggaagttt cccaaccatt 1800  
cccttatcca ggcttttga caacgctatg ctccgcgcccc atcgtctgca ccagctggcc 1860  
tttgacacctt accaggagtt tgaagaagcc tatatccaa aggaacagaa gtattcattc 1920  
ctgcagaacc cccagacctc cctctgtttc tcagagtcta ttccgacacc ctccaacagg 1980  
gaggaaacac aacagaaatc caacctagag ctgctccgca tctccctgct gctcatccag 2040  
tcgtggctgg agccctgtca gttcctcagg agtgtctcg ccaacagcct ggtgtacggc 2100  
gcctctgaca gcaacgtcta tgacctccta aaggacctag aggaaggcat ccaaacgctg 2160  
atggggaggc tggaaagatgg cagccccgg actgggcaga tcttcaagca gacctacagc 2220  
aagttcgaca caaactcaca caacgatgac gcactactca agaactacgg gctgctctac 2280  
tgcttcagga aggacatgga caaggtcgag acattcctgc gcatcgtgca gtgccgctct 2340  
gtggaggcga gctgtggctt cttaggatcc 2370

<210> 55  
<211> 786  
<212> PRT  
<213> Artificial

<220>  
<223> synthetic sequence

<220>  
<221> MISC\_FEATURE  
<222> (391)..(588)

<220>  
<221> mat\_peptide  
<222> (1)..()

<400> 55

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu  
1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe  
20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
180 185 190

Ser Trp Gly Gly Gly Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu  
195 200 205

Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe  
210 215 220

Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys  
225 230 235 240

Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser  
245 250 255

Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu  
260 265 270

Glu Leu Leu Arg Ile Ser Leu Leu Ile Gln Ser Trp Leu Glu Pro  
275 280 285

Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala  
290 295 300

Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile  
305 310 315 320

Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln  
325 330 335

Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp  
340 345 350

Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp  
355 360 365

Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val  
370 375 380

Glu Gly Ser Cys Gly Phe Ser Trp Gly Gly Gly Ser Phe Pro Thr  
385 390 395 400

Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala His Arg  
405 410 415

Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr  
420 425 430

Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser  
435 440 445

Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr  
450 455 460

Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Ile  
465 470 475 480

Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn  
485 490 495

Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys  
500 505 510

Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly  
515 520 525

Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp  
530 535 540

Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu  
545 550 555 560

Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile  
565 570 575

Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Ser Trp Gly Gly  
580 585 590

Gly Gly Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala  
595 600 605

Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln  
610 615 620

Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu  
625 630 635 640

Gln Asn Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro  
645 650 655

Ser Asn Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg  
660 665 670

Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu  
675 680 685

Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn  
690 695 700

Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met  
705 710 715 720

Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln  
725 730 735

Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu  
740 745 750

Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val  
755 760 765

Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys  
770 775 780

Gly Phe  
785

<210> 56  
<211> 33  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 56  
ttaccatgga ttgccggcgg cggcggatcc aat 33

<210> 57  
<211> 36  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 57  
ttaccatgga tttgatcagg cggcggcgg aat 36

<210> 58  
<211> 36

<212> DNA  
<213> Artificial  
  
<220>  
<223> synthetic sequence  
  
<400> 58  
tgatcaggcg gcggcggtac aggcggcggtc ggatcc

36

<210> 59  
<211> 10  
<212> PRT  
<213> Artificial  
  
<220>  
<223> synthetic sequence  
  
<400> 59

Ser Gly Gly Gly Ser Gly Gly Gly  
1 5 10

<210> 60  
<211> 48  
<212> DNA  
<213> Artificial  
  
<220>  
<223> synthetic sequence  
  
<400> 60  
gcggcggtcg gcggatcagg cggcggtcg tcaggcggtcg gggatcc

48

<210> 61  
<211> 14  
<212> PRT  
<213> Artificial  
  
<220>  
<223> synthetic sequence  
  
<400> 61  
  
Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly  
1 5 10  
  
<210> 62  
<211> 43  
<212> DNA  
<213> Artificial  
  
<220>  
<223> synthetic sequence  
  
<400> 62

ggacatatgc tgtgatcatt cccaaaccatt cccttatcca ggc

43

<210> 63  
<211> 41  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 63  
cgcgaaattcg atccatggaa gccacagctg ccctccacag a

41

<210> 64  
<211> 36  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 64  
cgcgtcgacc tagaagccac agctgccctc cacaga

36

<210> 65  
<211> 602  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 65  
catatgctgt gatcattccc aaccattccc ttatccaggc ttttgacaa cgctatgctc 60  
cgcgccatc gtctgcacca gctggccttt gacacctacc aggagttga agaagcctat 120  
atcccaaagg aacagaagta ttcatccctg cagaaccccc agacccctt ctgtttctca 180  
gagtctattc cgacaccctc caacagggag gaaacacaac agaaatccaa cctagagctg 240  
ctccgcattt ccctgctgtt catccagtcg tggctggagc ccgtcagtt cctcaggagt 300  
gtcttcgcca acagcctgggt gtacggcgcc tctgacagca acgtctatga cctcctaaag 360  
gacctagagg aaggcatcca aacgctgatg gggaggctgg aagatggcag ccccccggact 420  
gggcagatct tcaaggcagac ctacagcaag ttgcacacaa actcacacaa cgtgacgca 480  
ctactcaaga actacgggct gctctactgc ttgcacacaa actcacacaa cgtgacgca 540  
ttccctgcgca tcgtgcagtg ccgtctgtg gagggcagct gtggcttcca tggatcgaat 600  
tc 602

<210> 66  
<211> 192  
<212> PRT  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 66

Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu  
1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe  
20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
100 105 110

Asp Leu Leu Lys Asp Leu Glu Gly Ile Gln Thr Leu Met Gly Arg  
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
180 185 190

<210> 67  
<211> 600  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 67

catatgtgt	gatcattccc	aaccattccc	ttatccaggc	ttttgacaa	cgctatgct	60
cgccccatc	gtctgcacca	gctggcctt	gacacccattc	aggagttga	agaagcctat	120
atcccaaagg	aacagaagta	ttcattcctg	cagaaccccc	agacccct	ctgtttctca	180
gagtctattc	cgacaccctc	caacaggag	gaaacacaac	agaaaatccaa	cctagagctg	240
ctccgcatct	ccctgctgct	catccagtcg	tggctggagc	ccgtgcagtt	cctcaggagt	300
gtttcgcca	acagcctgg	gtacggcgcc	tctgacagca	acgtctatga	cctcctaaag	360
gacctagagg	aaggcatcca	aacgctgatg	gggaggctgg	aagatggcag	ccccggact	420
ggcagatct	tcaaggcagac	ctacagcaag	ttcgacacaa	actcacacaa	cgatgacgca	480
ctactcaaga	actacgggct	gctctactgc	ttcaggaagg	acatggacaa	ggtcgagaca	540
ttcctgcgca	tcgtgcagtg	ccgctctgtg	gagggcagct	gtggcttcta	ggtcgacgct	600

<210> 68  
 <211> 192  
 <212> PRT  
 <213> Artificial

<220>  
 <223> synthetic sequence

<400> 68

Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu  
 1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe  
 20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
 35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
 50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
 65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
 85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
 100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
 115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
 130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
180 185 190

<210> 69  
<211> 639  
<212> DNA  
<213> Artificial

<220>

<223> synthetic sequence

<400> 69  
catatgctgt gatcattccc aaccattccc ttatccaggc ttttgacaa cgctatgctc 60  
cgcgcccatc gtctgcacca gctggcctt gacacctacc aggagttga agaaggctat  
atcccaaagg aacagaagta ttcatccctg cagaaccccc agacctccct ctgtttctca 120  
gagtcttattc cgacaccctc caacaggag gaaacacaac agaaatccaa cctagagctg  
ctccgcatct ccctgctgct catccagtcg tggctggagc ccgtgcagtt cctcaggagt 180  
gtcttcgcca acagcctgggt gtacggcgcc tctgacagca acgtctatga cctcctaaag  
gacctagagg aaggcatcca aacgctgatg gggaggctgg aagatggcag ccccccggact 240  
gggcagatct tcaaggcagac ctacagcaag ttgcacacaa actcacacaa cgatgacgca  
ctactcaaga actacgggct gctctactgc ttcaaggaagg acatggacaa ggtcgagaca 300  
ttccctgcgca tcgtgcagtg ccgcctctgtg gagggcagct gtggcttcgg cggcggcgg 360  
tcaggcggcg gcggatcagg cggcggcggaa tccgaattc 420  
639

<210> 70  
<211> 206  
<212> PRT  
<213> Artificial

<220>

<223> synthetic sequence

<400> 70

Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu  
1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe  
20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
180 185 190

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly  
195 200 205

<210> 71

<211> 630

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<400> 71  
catatgttcc caaccattcc cttatccagg ctttttgaca acgctatgct ccgcggccat 60

cgtctgcacc agctggcctt tgacacctac caggagttt aagaaggccta tatcccaaag 120

gaacagaagt attcattcct gcagaacccc cagacccccc tctgtttctc agagtctatt 180

ccgacaccct ccaacaggg a gaaacacaa cagaaatcca accttagagct gctccgcattc 240

tccctgtgc tcattccagtc gtggctggag cccgtgcagt tcctcaggag tgtcttcgccc 300

aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag 360

gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc 420

ttcaaggaga	cctacagcaa	gttcgacaca	aactcacaca	acgatgacgc	actactcaag	480
aactacgggc	tgctctactg	cttcaggaag	gacatggaca	aggtcagac	attcctgcgc	540
atcgtgcagt	gccgctctgt	ggagggcagc	tgtggcttcg	gcggcggcgg	atcaggcggc	600
ggcgatcag	gcggcggcgg	atccgaattc				630

<210> 72  
<211> 206  
<212> PRT  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 72

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu  
1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe  
20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Val Tyr  
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
180 185 190

Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly  
195 200 205

<210> 73  
<211> 1248  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<220>  
<221> misc\_feature  
<222> (619)..(1236)  
<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 73  
tgatcattcc caaccattcc cttatccagg cttttgaca acgctatgct ccgcgcctat 60  
cgctgcacc agctggcctt tgacacctac caggagttt aagaagccta tatccaaag 120  
gaacagaagt attcattccgc cagaaccccc cagacctccc tctgtttctc agagtctatt 180  
ccgacaccct ccaacagggg gaaacacaaa cagaatcca acctagagct gctccgcac 240  
tccctgctgc tcattccagtc gtggctggag cccgtgcagt tcctcaggag tgtcttcgccc 300  
aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag 360  
gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tggcagatc 420  
ttcaaggcaga cctacagcaa gttcgacaca aactcacaca acgtgacgc actactcaag 480  
aactacgggc tgctctactg cttaggaag gacatggaca aggtcgagac attcctgcgc 540  
atcgtgcagt gccgctctgt ggagggcagc tgtggcttcg cggcggcgg atcaggcggc 600  
ggcgatcag cggcggcgg atcattccca accattccct tatccaggct tttgacaac 660  
gctatgctcc gcccacatcg tctgcaccag ctggccttg acacctacca ggagttgaa 720  
gaagcctata tccaaagga acagaagtat tcattcctgc agaacccca gacccctc 780  
tgtttctcag agtctattcc gacaccctcc aacagggagg aaacacaaca gaaatccaac 840  
ctagagctgc tccgcacatc cctgctgctc atccagtcgt ggctggagcc cgtgcagtcc 900  
ctcaggagtg tttcgccaa cagcctggtg tacggcgcct ctgacagacaa cgtctatgac 960  
ctcctaaagg acctagagga aggcacacaa acgctgatgg ggaggctgga agatggcagc 1020  
ccccggactg ggcagatctt caagcagacc tacagcaagt tcgacacaaa ctcacacaaac 1080  
gatgacgcac tactcaagaa ctacgggctg ctctactgct tcaggaagga catggacaag 1140  
gtcgagacat tcctgcgcac cgtgcagtgc cgctctgtgg agggcagctg tggcttcggc 1200

ggcgccggat caggcggcgg cggatcaggc ggcggccggat ccgaattc

1248

<210> 74

<211> 412

<212> PRT

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> MISC\_FEATURE

<222> (193)..(398)

<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 74

Ser Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu  
1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe  
20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
180 185 190

Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Phe

195

200

205

Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala  
210 215 220

His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu  
225 230 235 240

Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln  
245 250 255

Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu  
260 265 270

Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu  
275 280 285

Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe  
290 295 300

Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu  
305 310 315 320

Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu  
325 330 335

Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys  
340 345 350

Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly  
355 360 365

Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu  
370 375 380

Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Gly Gly  
385 390 395 400

Gly Gly Ser Gly Gly Ser Gly Gly Gly  
405 410

<210> 75

<211> 2445

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> misc\_feature

<222> (1237)..(1854)

<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 75

catatgttcc caaccattcc cttatccagg cttttgaca acgctatgct ccgcgcctat 60  
cgctgcacc agctggcctt tgacacctac caggagttt aagaaggcta tatcccaaag 120  
gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt 180  
ccgacacccct ccaacagggaa ggaaacacaa cagaaatcca acctagagct gctccgcata 240  
tccctgctgc tcatccagtc gtggctggag cccgtgcagt tcctcaggag tgtcttcgccc 300  
aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag 360  
gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tggcagatc 420  
ttcaaggcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag 480  
aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc 540  
atcgtgcagt gccgcctgtt ggagggcagc tgtggcttcg gccggcggcgg atcaggcggc 600  
ggcggatcag gccggcggcgg atcattccca accattccct tatccaggct ttttgacaac 660  
gctatgctcc gcccgcattcg tctgcaccag ctggcctttg acacctacca ggagttgaa 720  
gaagcctata tcccaaagga acagaagtat tcattcctgc agaaccccca gacccctc 780  
tgtttctcag agtctattcc gacaccctcc aacagggagg aaacacaaca gaaatccaaac 840  
ctagagctgc tccgcatttc cctgctgctc atccagtcgt ggctggagcc cgtgcagttc 900  
ctcaggagtg tcttcgccaa cagcctggtg tacggcgcct ctgacagcaa cgtctatgac 960  
ctcctaaagg acctagagga aggcatccaa acgctgatgg ggaggctgaa agatggcagc 1020  
ccccggactg ggcagatctt caagcagacc tacagcaagt tcgacacaaa ctcacacaac 1080  
gatgacgcac tactcaagaa ctacgggctg ctctactgct tcaggaagga catggacaag 1140  
gtcgagacat tcctgcgcatt cgtgcagtc cgctctgtgg agggcagctg tggcttcggc 1200  
ggcggcggat caggcggcgg cggatcagggc ggcggcggat cattcccaac cattccctta 1260  
tccaggctt ttgacaacgc tatgctccgc gcccattcgctc tgccaccagct ggcctttgac 1320  
acctaccagg agtttgaaga agcctatatac ccaaaggaaac agaagtattc attcctgcag 1380  
aaccccccaga cctccctctg tttctcagag tctattccga caccctccaa cagggaggaa 1440  
acacaacaga aatccaaacct agagctgctc cgcattccctc tgctgctcat ccagtcgtgg 1500  
ctggagcccg tgcagttcct caggagtgtc ttgcacaaca gcctgggtga cggcgcctct 1560  
gacagcaacg tctatgaccc cctaaaggac ctagaggaag gcatccaaac gctgatgggg 1620  
aggctggaag atggcagccc cggactggg cagatctca agcagaccta cagcaagtcc 1680  
gacacaaact cacacaacga tgacgcacta ctcaagaact acgggctgct ctactgcttc 1740

aggaaggaca tggacaaggc cgagacattc ctgcgcacatcg tgcagtgcgg ctctgtggag 1800  
ggcagctgtg gcttcggcgg cggcgatca ggcggcggcg gatcaggcgg cggcgatca 1860  
ttcccaacca ttcccttatac caggctttt gacaacgcta tgctccgcgc ccacatcgatcg 1920  
caccagctgg ccttgacac ctaccaggag tttgaagaag cctatatccc aaaggaacag 1980  
aagtattcat tcctgcagaa ccccccagacc tccctctgtt tctcagatgc tattccgaca 2040  
ccctccaaca gggagggaaac acaacagaaa tccaaacctag agctgctccg catctccctg 2100  
ctgctcatcc agtcgtggct ggagccccgtg cagttcctca ggagtgtctt cgccaaacagc 2160  
ctgggtgtacg gcgcctctga cagcaacgtc tatgacctcc taaaggacct agaggaaggc 2220  
atccaaacgc tcatggggag gcttgaagat ggcagcccc ggactggca gatcttcaag 2280  
cagacctaca gcaagttcga cacaactca cacaacgtg acgactact caagaactac 2340  
ggctgctct actgcttcag gaaggacatg gacaaggctg agacattcct gcgcacatcg 2400  
cagtggcgct ctgtggaggg cagctgtggc ttcttaggtcg acgctg 2445

<210> 76  
<211> 810  
<212> PRT  
<213> Artificial

<220>  
<223> synthetic sequence

<220>  
<221> MISC\_FEATURE  
<222> (412)..(617)  
<223> sequence is repeated N-1 times, where N is a positive whole number

<220>  
<221> mat\_peptide  
<222> (1)..()

<400> 76

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu  
1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe  
20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn

50

55

60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
180 185 190

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Phe  
195 200 205

Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala  
210 215 220

His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu  
225 230 235 240

Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln  
245 250 255

Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu  
260 265 270

Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu  
275 280 285

Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe  
290 295 300

Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu  
305 310 315 320

Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu  
325 330 335

Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys  
340 345 350

Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly

355

360

365

Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu  
370 375 380

Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Gly Gly  
385 390 395 400

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Phe Pro Thr  
405 410 415

Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala His Arg  
420 425 430

Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr  
435 440 445

Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser  
450 455 460

Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr  
465 470 475 480

Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Ile  
485 490 495

Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn  
500 505 510

Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys  
515 520 525

Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly  
530 535 540

Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp  
545 550 555 560

Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu  
565 570 575

Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile  
580 585 590

Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe Gly Gly Gly  
595 600 605

Ser Gly Gly Gly Ser Gly Gly Ser Phe Pro Thr Ile Pro  
610 615 620

Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His  
625 630 635 640

Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro  
645 650 655

Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys

660

665

670

Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln  
 675 680 685

Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser  
 690 695 700

Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu  
 705 710 715 720

Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu  
 725 730 735

Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro  
 740 745 750

Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn  
 755 760 765

Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys  
 770 775 780

Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln  
 785 790 795 800

Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
 805 810

<210> 77

<211> 593

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<400> 77

catatgttcc caaccattcc cttatccagg ctttttgaca acgctatgct ccgcgcctat 60

cgtctgcacc agctggcctt tgacacctac caggagttt aagaagccta tatcccaaag 120

gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt 180

ccgacaccct ccaacaggga ggaaacacaa cagaaatcca accttagagct gctccgcattc 240

tccctgctgc tcatccagtc gtggctggag cccgtgcagt tcctcaggag tgtcttcgcc 300

aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag 360

gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc 420

ttcaagcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag 480

aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc 540

atcgtgcagt gccgctctgt ggagggcagc tgtggcttcc atggatcgaa ttc 593

<210> 78  
<211> 192  
<212> PRT  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 78

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu  
1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe  
20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
180 185 190

<210> 79  
<211> 592  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 79

aagtttccc aaccattccc ttatccaggc ttttgacaa cgctatgctc cgcccccac	60
gtctgcacca gctggcctt gacacctacc aggagttga agaagcctat atcccaaagg	120
aacagaagta ttcattcctg cagaaccccc agacccctt ctgttctca gagtctattc	180
cgacaccctc caacaggag gaaacacaac agaaatccaa ccttagagctg ctccgcacatct	240
ccctgctgct catccagtcg tggctggagc ccgtgcagtt cctcaggagt gtttcgcca	300
acagcctgggt gtacggcgcc tctgacagca acgtctatga cctcctaaag gacctagagg	360
aaggcatcca aacgctgatg gggaggctgg aagatggcag ccccccggact gggcagatct	420
tcaagcagac ctacagcaag ttgcacacaa actcacacaa cgatgacgca ctactcaaga	480
actacgggct gctctactgc tttaggaagg acatggacaa ggtcgagaca ttctcgca	540
tcgtgcagtg ccgctctgtg gagggcagct gtggcttcca tggatcgaat tc	592

<210> 80

<211> 191

<212> PRT

<213> Artificial

<220>

<223> synthetic sequence

<400> 80

Phe	Pro	Thr	Ile	Pro	Leu	Ser	Arg	Leu	Phe	Asp	Asn	Ala	Met	Leu	Arg
1				5				10					15		

Ala	His	Arg	Leu	His	Gln	Leu	Ala	Phe	Asp	Thr	Tyr	Gln	Glu	Phe	Glu
			20				25					30			

Glu	Ala	Tyr	Ile	Pro	Lys	Glu	Gln	Lys	Tyr	Ser	Phe	Leu	Gln	Asn	Pro
			35			40					45				

Gln	Thr	Ser	Leu	Cys	Phe	Ser	Glu	Ser	Ile	Pro	Thr	Pro	Ser	Asn	Arg
			50		55				60						

Glu	Glu	Thr	Gln	Gln	Lys	Ser	Asn	Leu	Glu	Leu	Leu	Arg	Ile	Ser	Leu
			65		70			75				80			

Leu	Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln	Phe	Leu	Arg	Ser	Val
				85			90				95				

Phe	Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr	Asp
				100		105						110			

Leu	Leu	Lys	Asp	Leu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Gly	Arg	Leu
			115		120						125			

Glu	Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	Lys	Gln	Thr	Tyr	Ser
				130		135			140						

Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr  
145 150 155 160

Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe  
165 170 175

Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
180 185 190

<210> 81  
<211> 587  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 81  
aagtttccc aaccattccc ttatccaggc ttttgacaa cgctatgctc cgcccccattc 60  
gtctgcacca gctggccttt gacacctacc aggagttga agaagcctat atcccaaagg  
aacagaagta ttcattcctg cagaacccccc agacccctt ctgtttctca gagtctattc 120  
cgacaccctc caacaggag gaaacacaac agaaatccaa ccttagagctg ctccgcacatct 180  
ccctgctgct catccagtcg tggctggagc ccgtgcagtt cctcaggagt gtcttcgcctt 240  
acagcctgggt gtacggcgcc tctgacagca acgtctatga cctcctaaag gacctagagg 300  
aaggcatcca aacgctgatg gggaggctgg aagatggcag ccccccggact gggcagatct 360  
tcaaggcagac ctacagcaag ttcgacacaa actcacacaa cgatgacgca ctactcaaga 420  
actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca ttccctgcgca 480  
tcgtgcagtg ccgctctgtg gagggcagct gtggcttcta gggatcc 540  
587

<210> 82  
<211> 191  
<212> PRT  
<213> Artificial

<220>  
<223> synthetic sequence

<400> 82

Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg  
1 5 10 15

Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu  
20 25 30

Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro

35

40

45

Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg  
 50 55 60

Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu  
 65 70 75 80

Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val  
 85 90 95

Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp  
 100 105 110

Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu  
 115 120 125

Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser  
 130 135 140

Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr  
 145 150 155 160

Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe  
 165 170 175

Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
 180 185 190

<210> 83

<211> 1165

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> misc\_feature

<222> (579)..(1151)

<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 83

aagctttccc aaccattccc ttatccaggc tttttgacaa cgctatgctc cgcgccatc 60

gtctgcacca gctggcctt gacacctacc aggagttga agaaggctat atcccaaagg 120

aacagaagta ttcattcctg cagaaccccc agacccctt ctgtttctca gagtctattc 180

cgacaccctc caacagggag gaaacacaac agaaatccaa cctagagctg ctccgcattc 240

ccctgctgct catccagtcg tggctggagc ccgtgcagtt cctcaggagt gtcttcgcca 300

acagcctggcgt acgtctatga cctcctaaag gacctagagg 360

aaggcatcca aacgctgatg	420
gggaggctgg aagatggcag	
ccccggact gggcagatct	
tcaaggcagac ctacagcaag	480
ttcgacacaa actcacacaa	
cgatgacgca ctactcaaga	
actacgggct gctctactgc	540
ttcaggaagg acatggacaa	
ggtcgagaca ttcctgcgca	
tcgtgcagtg ccgctctgtg	600
gagggcagct gtggcttctt	
cccaaccatt cccttatcca	
ggcttttga caacgctatg	660
ctccgcgccc atcgtctgca	
ccagctggcc tttgacacct	
accaggagtt tgaagaagcc	720
tatatccaa aggaacagaa	
gtattcattc ctgcagaacc	
cccagacctc cctctgttcc	780
tcagagtcta ttccgacacc	
ctccaacagg gaggaacac	
aacagaaatc caacctagag	840
ctgctccgca tctccctgct	
gctcatccag tcgtggctgg	
agcccggtgca gttcctcagg	900
agtgtctcg ccaacagcct	
ggtgtacggc gcctctgaca	
gcaacgtcta tgacccctta	960
aaggacctag aggaaggcat	
ccaaacgctg atggggaggc	
tggaagatgg cagccccgg	1020
actggcaga tcttcaagca	
gacctacagc aagttcgaca	
caaactcaca caacgatgac	1080
gcactactca agaactacgg	
gctgctctac tgcttcagga	
aggacatgga caaggtcgag	1140
acattcctgc gcatcgtgca	
gtgccgctct gtggagggca	
gctgtggctt ccatggatcg	
aattc	1165

<210> 84

<211> 191

<212> PRT

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> MISC\_FEATURE

<222> (1)..(191)

<223> sequence is repeated N times, where N is a positive whole number

<400> 84

Phe	Pro	Thr	Ile	Pro	Leu	Ser	Arg	Leu	Phe	Asp	Asn	Ala	Met	Leu	Arg
1					5				10				15		

Ala	His	Arg	Leu	His	Gln	Leu	Ala	Phe	Asp	Thr	Tyr	Gln	Glu	Phe	Glu
							20		25			30			

Glu	Ala	Tyr	Ile	Pro	Lys	Glu	Gln	Lys	Tyr	Ser	Phe	Leu	Gln	Asn	Pro
								35		40		45			

Gln	Thr	Ser	Leu	Cys	Phe	Ser	Glu	Ser	Ile	Pro	Thr	Pro	Ser	Asn	Arg
								50		55		60			

Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu  
65 70 75 80

Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser Val  
85 90 95

Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp  
100 105 110

Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg Leu  
115 120 125

Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser  
130 135 140

Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr  
145 150 155 160

Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe  
165 170 175

Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
180 185 190

<210> 85

<211> 2307

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> misc\_feature

<222> (1153)..(1725)

<223> sequence is repeated N-1 times, where N is a positive whole number

<400> 85

catatgttcc caaccattcc cttatccagg cttttgaca acgctatgct ccgcgcctat 60

cgtctgcacc agctggcctt tgacacctac caggagttt aagaaggcta tatcccaaag 120

gaacagaagt attcattcct gcagaacccc cagacctccc tctgtttctc agagtctatt 180

ccgacacccct ccaacaggg a gaaacacaa cagaaatcca acctagagct gctccgcata 240

tccctgctgc tcattccagtc gtggctggag cccgtgcagt tcctcaggag tgtcttcgccc 300

aacagcctgg tgtacggcgc ctctgacagc aacgtctatg acctcctaaa ggacctagag 360

gaaggcatcc aaacgctgat ggggaggctg gaagatggca gccccggac tgggcagatc 420

ttcaaggcaga cctacagcaa gttcgacaca aactcacaca acgatgacgc actactcaag 480

aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgccc 540  
atcgtgcagt gcccgtctgt ggagggcagc tgtggcttct tcccaaccat tcccttatcc 600  
aggcttttg acaacgctat gctccgccc catcgctgc accagctggc ctttgacacc 660  
taccaggagt ttgaagaagc ctatatccca aaggaacaga agtattcatt cctgcagaac 720  
ccccagacct ccctctgttt ctcagagtct attccgacac cctccaacag ggagggaaaca 780  
caacagaaat ccaacctaga gctgctccgc atctccctgc tgctcatcca gtcgtggctg 840  
gagcccgtgc agttccctag gagtgcttc gccaacagcc tgggtacgg cgccctctgac 900  
agcaacgtct atgacccctt aaaggaccta gaggaaggca tccaaacgct gatggggagg 960  
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acaaactcac acaacgatga cgcaactactc aagaactacg ggctgctcta ctgcttcagg 1080  
aaggacatgg acaaggtcga gacattcctg cgcatcggtc agtgcgcgtc tgtggaggc 1140  
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gcccatcgtc tgccaccagct ggcccttgac acctaccagg agtttgaaga agcctatata 1260  
ccaaaggaac agaagtattc attcctgcag aaccccaaga cctccctctg tttctcagag 1320  
tctattccga caccctccaa cagggaggaa acacaacaga aatccaaacct agagctgctc 1380  
cgcatctccc tgctgctcat ccagtcgtgg ctggagcccg tgcaaggctt caggagtgtc 1440  
ttcgccaaca gcctgggtta cggcgccctct gacagcaacg tctatgacct cctaaaggac 1500  
ctagaggaag gcatccaaac gctgatgggg aggctggaag atggcagccc ccggactggg 1560  
cagatctca agcagaccta cagcaagttc gacacaaact cacacaacga tgacgcacta 1620  
ctcaagaact acgggctgct ctactgcttc aggaaggaca tggacaaggc cgagacattc 1680  
ctgcccattcg tgcaagtggcg ctctgtggag ggcagctgtg gcttcttccc aaccattccc 1740  
ttatccaggg ttttgacaa cgctatgctc cgcccccattc gtctgcacca gctggccctt 1800  
gacacccattcaggatgttga agaaggctat atcccaaagg aacagaagta ttcatttctg 1860  
cagaacccccc agaccccttctca gagtctattc cgacaccctc caacagggag 1920  
gaaacacaaac agaaatccaa cctagagctg ctccgcattt ccctgctgct catccagtcg 1980  
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tctgacagca acgtctatga cttccctaaag gacctagagg aaggcatcca aacgctgatg 2100  
gggaggctgg aagatggcag ccccccggact gggcagatct tcaaggcagac ctacagcaag 2160  
ttcgacacaaactcacacaa cgatgacgca ctactcaaga actacgggct gctctactgc 2220

ttcaggaagg acatggacaa ggtcgagaca ttccctgcgca tcgtgcagtg ccgctctgtg 2280

gagggcagct gtggcttcta gggatcc 2307

<210> 86

<211> 192

<212> PRT

<213> Artificial

<220>

<223> synthetic sequence

<220>

<221> MISC\_FEATURE

<222> (2)...(192)

<223> sequence is repeated N+2 times, where N is a positive whole number

<220>

<221> mat\_peptide

<222> (1)...()

<400> 86

Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu  
1 5 10 15

Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe  
20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn  
35 40 45

Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn  
50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser  
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser  
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr  
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg  
115 120 125

Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
130 135 140

Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn  
145 150 155 160

Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr  
165 170 175

Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe  
180 185 190